

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Kim, Yesook
 Lambert, William J.
 Qi, Hong
 Gelfand, Robert A.
 Geoghegan, Kieran F.
 Danley, Dennis E.
- 10 (ii) TITLE OF INVENTION: Prolonged Delivery of Peptides
- 15 (iii) NUMBER OF SEQUENCES: 7
- 15 (iv) CORRESPONDENCE ADDRESS:
 (A) ADDRESSEE: Pfizer Inc
 (B) STREET: 235 East 42nd Street, 20th Floor
 (C) CITY: New York
 (D) STATE: New York
20 (E) COUNTRY: U.S.A.
 (F) ZIP: 10017-5755
- 25 (v) COMPUTER READABLE FORM:
 (A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- 30 (vi) CURRENT APPLICATION DATA:
 (A) APPLICATION NUMBER:
 (B) FILING DATE:
 (C) CLASSIFICATION:
- 35 (viii) ATTORNEY/AGENT INFORMATION:
 (A) NAME: Sheyka, Robert F.
 (B) REGISTRATION NUMBER: 31,304
 (C) REFERENCE/DOCKET NUMBER: PC8391
- 40 (ix) TELECOMMUNICATION INFORMATION:
 (A) TELEPHONE: (212)573-1189
 (B) TELEFAX: (212)573-1939
 (C) TELEX: N/A
- 45 (2) INFORMATION FOR SEQ ID NO:1:
- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
50 (D) TOPOLOGY: linear
- 55 (ii) MOLECULE TYPE: peptide
- 55 (iii) HYPOTHETICAL: NO
- 55 (iv) ANTI-SENSE: NO
- 55 (v) FRAGMENT TYPE: N-terminal
- 60 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: N/A
 (B) STRAIN: N/A
 (C) INDIVIDUAL ISOLATE: N/A
 (E) HAPLOTYPE: N/A

(H) CELL LINE: N/A

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: N/A
(B) CLONE: N/A

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(viii) POSITION IN GENOME:

- (A) CHROMOSOME SEGMENT: N/A
(B) MAP POSITION: N/A
(C) UNITS: N/A

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

His Asp Glu Phe Glu Arg His Ala Glu Gly Thr Phe Thr Ser Asp Val
1 5 10 15

Ser Ser Tyr Leu Glu Gly Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu
20 25 30

20 Val Lys Gly Arg Gly
35

(2) INFORMATION FOR SEQ ID NO:2:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

35 (iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

40 (vi) ORIGINAL SOURCE:
(A) ORGANISM: N/A
(B) STRAIN: N/A
(C) INDIVIDUAL ISOLATE: N/A
(E) HAPLOTYPE: N/A
(H) CELL LINE: N/A

45 (vii) IMMEDIATE SOURCE:
(A) LIBRARY: N/A
(B) CLONE: N/A

50 (viii) POSITION IN GENOME:
(A) CHROMOSOME SEGMENT: N/A
(B) MAP POSITION: N/A
(C) UNITS: N/A

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

His Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly
1 5 10 15

60 Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly
20 25 30

(2) INFORMATION FOR SEQ ID NO:3:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 10 (ii) MOLECULE TYPE: peptide
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
15 (v) FRAGMENT TYPE: N-terminal
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: N/A
 (B) STRAIN: N/A
20 (C) INDIVIDUAL ISOLATE: N/A
 (E) HAPLOTYPE: N/A
 (H) CELL LINE: N/A
 (vii) IMMEDIATE SOURCE:
25 (A) LIBRARY: N/A
 (B) CLONE: N/A
 (viii) POSITION IN GENOME:
30 (A) CHROMOSOME SEGMENT: N/A
 (B) MAP POSITION: N/A
 (C) UNITS: N/A
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
35 His Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly
 1 5 10 15
- 40 Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg
 20 25 30

40 (2) INFORMATION FOR SEQ ID NO:4:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 50 (ii) MOLECULE TYPE: peptide
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
55 (v) FRAGMENT TYPE: N-terminal
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: N/A
 (B) STRAIN: N/A
60 (C) INDIVIDUAL ISOLATE: N/A
 (E) HAPLOTYPE: N/A
 (H) CELL LINE: N/A

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: N/A
(B) CLONE: N/A

5 (viii) POSITION IN GENOME:
(A) CHROMOSOME SEGMENT: N/A
(B) MAP POSITION: N/A

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
His Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly
1 5 10 15

15 Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly
20 25

(2) INFORMATION FOR SEQ ID NO:5:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

30 (iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

35 (vi) ORIGINAL SOURCE:
(A) ORGANISM: N/A
(B) STRAIN: N/A
(C) INDIVIDUAL ISOLATE: N/A
(E) HAPLOTYPE: N/A
(H) CELL LINE: N/A

40 (vii) IMMEDIATE SOURCE:
(A) LIBRARY: N/A
(B) CLONE: N/A

45 (viii) POSITION IN GENOME:
(A) CHROMOSOME SEGMENT: N/A
(B) MAP POSITION: N/A

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
His Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly
1 5 10 15

55 Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys
20 25

(2) INFORMATION FOR SEQ ID NO:6:

60 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

5 (iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

10 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: N/A
- (B) STRAIN: N/A
- (C) INDIVIDUAL ISOLATE: N/A
- (E) HAPLOTYPE: N/A
- (H) CELL LINE: N/A

15 (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: N/A
- (B) CLONE: N/A

20 (viii) POSITION IN GENOME:

- (A) CHROMOSOME SEGMENT: N/A
- (B) MAP POSITION: N/A

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

His Asp Glu Phe Glu Arg His Ala Glu Gly Thr Phe Thr Ser Asp Val
1 5 10 15

30 Ser Ser Tyr Leu Glu Gly Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu
20 25 30

Val Lys Gly Arg
35

35 (2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: peptide

45 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

50 (v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N/A
- (B) STRAIN: N/A
- (C) INDIVIDUAL ISOLATE: N/A
- (E) HAPLOTYPE: N/A
- (H) CELL LINE: N/A

55 (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: N/A
- (B) CLONE: N/A

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(viii) POSITION IN GENOME:

- (A) CHROMOSOME SEGMENT: N/A
- (B) MAP POSITION: N/A

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

His Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly
1 5 10 15

10 Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val
20 25